SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: KAYAGAKI, Nobuhiko YAGITA, Kideo

OKUMURA, Ko

NAKATA, Motomi

(ii) TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFICALLY
REACTING WITH Fas LIGAND AND PRODUCTION PROCESS THEREOF

(iii) NUMBER OF SEQUENCES: 31

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: McDermott, Will & Emery
- (B) STREET: 99 Canal Center Plaza, Suite 300
- (C) CITY: Alexandria
- (D) STATE: Virginia
- (E) COUNTRY: USA
- (F) ZIP: 22314

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: US 08/913,555
- (B) FILING DATE: 19-SEP-1997
- (C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Bucca Ph.D., Daniel
- (B) REGISTRATION NUMBER: 42,368
- (C) REFERENCE/DOCKET NUMBER: 50356-150

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 202-756-8600
- (B) TELEFAX: 202-756-8699

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 120 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Val Gln Leu Gln Glu Ser Gly Pro Glu Leu Val Lys Pro Gly Ala Ser
1 5 10 15

Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Trp

Met Asn Trp Val Lys Gln Arg Pro Gly Lys Gly Leu Glu Trp Ile Gly 35 40 45

Arg Ile Tyr Pro Gly Asp Gly Asp Thr Asn Asp Asn Gly Lys Phe Lys 50 55 60	
Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met 65 70 75 80	
Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala 85 90 95	
Arg Ser Tyr Tyr Tyr Asp Gly Ser Pro Trp Phe Thr Tyr Trp Gly Gln 100 105 110	
Gly Thr Thr Val Thr Val Ser Ser 115 120	
(2) INFORMATION FOR SEQ ID NO:2:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 360 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA to mRNA	
(xi) SEQUENCE DESCRIPTION: SEO ID NO:2:	
	50
TGCAAGGCTT CTGGCTATGC ATTCAGTAGC TCCTGGATGA ACTGGGTGAA GCAGAGGCCT 12	
GGAAAGGGTC TTGAGTGGAT TGGACGAATT TATCCTGGAG ATGGAGATAC TAACGACAAC 18	30
GGGAAGTTCA AGGGCAAGGC CACACTGACC GCAGACAAAT CCTCCAGCAC AGCCTACATG 24	ł O
CAACTCAGCA GTCTGACATC TGAGGACTCT GCGGTCTACT TCTGTGCAAG ATCGTATTAC 30	0 0
TACGATGGTA GCCCCTGGTT TACTTACTGG GGCCAAGGGA CCACGGTCAC CGTCTCCTCA 36	50
(2) INFORMATION FOR SEQ ID NO:3:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 108 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: peptide	
(wi) GEOMENGE DECERTIFIED, GEO. ID NO. 2	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:	
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly 1 5 10	
Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Asn Tyr 20 25 30	
Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile 35 40 45	

	Tyr	Tyr 50	Thr	Ser	Arg	Leu	His 55	Ser	Gly	Val	Pro	Ser 60	Arg	Phe	Ser	Gly	
	Ser 65	Gly	Ser	Gly	Thr	Asp 70	Tyr	Ser	Leu	Thr	Ile 75	Ser	Asn	Leu	Glu	Pro 80	
	Glu	Asp	Ile	Ala	Thr 85	Tyr	Phe	Cys	Gln	Gln 90	Tyr	Ser	Glu	Phe	Pro 95	Trp	
	Thr	Phe	Gly	Gly 100	Gly	Thr	Lys	Leu	Glu 105	Ile	Lys	Arg					
(2)	INFO	RMAT	ION 1	FOR S	SEQ :	ID NO	0:4:										
	(i)	(A) (B) (C)	LEI TYI STI	NGTH PE: 1 RANDI	ARACT : 324 nucle EDNES	1 bas eic a SS: c	se pa acid doubl	airs									
	(ii)	MOLE	ECULI	E TYI	PE: 0	DNA	to m	nRNA									
	(xi)	SEQU	JENCI	E DES	SCRIE	OITS	N: SE	EQ II	ON C	4:							
GACA	TCCA	GA TO	GACG	CAGT	TCC	CATC	CTCC	CTGT	CTG	CCT (CTCTC	GGA	BA CA	AGAGT	CAC	2	60
ATCA	GTTG	CA GO	GCA	AGTC	A GGA	TAT	ragc	AATT	TTTAT	TAA A	ACTGO	TAT	CA GO	CAGA	AACC	A	120
GATO	GAAC:	rg T	raaa(CTCC:	r gan	CTAC	CTAC	ACAT	CAAC	AT T	CACAC	CTCAC	G A	TCCC	CATC	A	180
AGGI	TCAG:	rg go	CAGT	GGT	C TGC	GAC	AGAT	TATT	CTC	CA (CCATO	CAGCA	AA C	CTGG	AACC'	ľ	240
GAAG	TATA	rg co	CACT	ract:	r TTC	STCAC	GCAA	TATA	AGTGI	TA	TCCC	TGG	AC GI	TCGC	GTGG <i>I</i>	A	300
GGCA	CCAA	GC TO	GAA	ATCA	A ACC	GG											324
(2)	INFO	TAMS	ON I	FOR S	SEQ I	D NO	D:5:										
	(i)	(A) (B) (C)	LEN TYI	NGTH PE: 6 RANDI	ARACT : 118 amino EDNES GY:]	3 ami 5 aci 5S: s	ino a id singl	acids	3								
	(ii)	MOLE	ECULI	E TYI	PE: I	pepti	ide										
						٠											
	(xi)	SEQU	JENCI	E DES	SCRIE	OITS	1: SI	EQ II	NO:	:5:							
	Val 1	Gln	Leu	Gln	Gln 5	Ser	Gly	Ala	Glu	Leu 10	Val	Arg	Pro	Gly	Thr 15	Ser	
	Val	Lys	Met	Ser 20	Cys	Lys	Ala	Ala	Gly 25	Tyr	Thr	Phe	Thr	Asn 30	Tyr	Trp	
	Ile	Gly	Trp 35	Val	Lys	Gln	Arg	Pro 40	Gly	His	Gly	Leu	Glu 45	Trp	Ile	Gly	
	Tyr	Leu 50	Tyr	Pro	Gly	Gly	Leu 55	Tyr	Thr	Asn	Tyr	Asn 60	Glu	Lys	Phe	Lys	
	Gly	Lys	Ala	Thr	Leu	Thr	Ala	Asp	Thr	Ser	Ser	Ser	Thr	Ala	Tyr	Met	

65					70					75					80	
Gln	Leu	Ser	Ser	Leu 85	Thr	Ser	Glu	Asp	Ser 90	Ala	Ile	Tyr	Tyr	Cys 95	Ala	
Arg	Tyr	Arg	Asp 100	Tyr	Asp	Tyr	Ala	Met 105	Asp	Tyr	Trp	Gly	Gln 110	Gly	Thr	
Thr	Val	Thr 115	Val	Ser	Ser											
(2) INFO	RMATI	ON E	FOR S	SEQ 1	D NO	0:6:										
(i)	(B)	JENCE LEN TYE STE TOE	GTH: PE: r RANDE	: 354 nucle EDNES	bas ic a SS: c	se pa acid loubl	airs									
(ii)	MOLE	CULE	E TYP	PE: c	DNA	to r	nRNA									
(xi)	SEQU	JENCI	E DES	SCRIE	TION	N: SE	EO II	NO:	6:							
GTGCAGCT	GC AC	3CAGT	CAGO	ago	CTGAC	GCTG	GTA	AGGCC	CTG (GACI	TCAC	FT G	AAGAT	rgtco	2	60
TGCAAGGC'	rg Ci	rgga:1	racac	CTI	CAC	TAAC	TACT	rggai	rag (TTGG	GTA	AA G	CAGAC	GCCT	ŗ	120
GGACATGG	CC TI	rgag1	rggai	r TG0	ATA	CTT	TACC	CCTGC	AG (TCTI	TAT	AC TA	AACTA	ACAAT	r	180
GAGAAGTT	CA AC	GGCF	AAGGC	CAC	CACTO	ACT	GCAC	BACAC	CAT (CCTCC	CAGC	AC AC	GCTA	CATO	3	240
CAGCTCAG	CA GO	CTGF	ACATO	C TGA	AGGA	CTCT	GCC	ATCT <i>I</i>	ATT A	ACTGI	GCA	AG A	racac	GGAI	r	300
TACGACTA	IG CI	ATG	GACTA	A CTC	GGGG	CCAA	GGG	ACCAC	CGG T	CACC	GTCI	rc cr	ГСА			354
(2) INFO	RMATI	ON F	FOR S	SEQ 1	D NO):7:										
(i)	(B) (C)	JENCE LEN TYE STE TOE	NGTH: PE: a RANDE	: 113 amino EDNES	ami aci SS: s	ino a id singl	acids	5								
(ii)	MOLE	CULE	E TYP	E: p	epti	de										
(xi)	SEQU	IENCE	z DES	SCR T F	ארדית	J. SF	70 TI	NO.	7.							
	Val						-			T.eu	Pro	Val	Asn	Tle	Glv	
1				5					10					15	1	
Asp	Gln	Ala	Ser 20	Ile	Ser	Cys	Lys	Ser 25	Thr	Lys	Ser	Leu	Leu 30	Asn	Ser	
Asp	Gly	Phe 35	Thr	Tyr	Leu	Gly	Trp 40	Cys	Leu	Gln	Lys	Pro 45	Gly	Gln	Ser	

Pro Gln Leu Leu Ile Tyr Leu Val Ser Asn Arg Phe Ser Gly Val Pro

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile 70 75 80

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Phe Glr 85 90 95	ı Ser
Asn Tyr Leu Pro Leu Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile 100 105 110	: Lys
Arg	
(2) INFORMATION FOR SEQ ID NO:8:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 339 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA to mRNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:	
GATGTTTTGA TGACCCAAAC TCCACTCTCT CTGCCTGTCA ATATTGGAGA TCAAGCCTC	
ATCTCTTGCA AGTCTACTAA GAGCCTTCTG AATAGTGATG GATTCACTTA TTTGGGCTC	
TGCCTGCAGA AGCCAGGCCA GTCTCCACAG CTCCTAATAT ATTTGGTTTC TAATCGATT	
TCTGGAGTTC CAGACAGGTT CAGTGGTAGT GGGTCAGGGA CAGATTTCAC CCTCAAGAT	
AGCAGAGTGG AGGCTGAGGA TTTGGGGAGTT TATTATTGCT TCCAGAGTAA CTATCTTCC	
CTTACGTTCG GATCGGGGAC CAAGCTGGAA ATAAAACGG	339
(2) INFORMATION FOR SEQ ID NO:9:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 116 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: peptide	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:	
Val Lys Leu Gln Glu Ser Gly Pro Glu Leu Val Lys Pro Gly Ala 1 5 10 15	ı Ser
Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Ser 20 25 30	Trp
Met Asn Trp Val Lys Gln Arg Pro Gly Lys Gly Leu Glu Trp Ile 35 40 45	: Gly
Arg Ile Tyr Pro Val Asn Gly Asp Thr Asn Tyr Asn Gly Lys Phe	: Lys
Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr 65 70 75	Met 80
Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys	Ala

Thr	Asp	Gly	Tyr	Trp	Tyr	Phe	Asp	Val	Trp	Gly	Gln	Gly	Thr	Thr	Val
			100					105					110		

Thr Val Ser Ser 115

(2)	INFORMATION	FOR	SEO	TD	NO.	10

(i)	CECTIENCE	CHARACTERISTICS
$\iota \perp \iota$	SP.OUP.NUE.	CHARACTERISTICS

- (A) LENGTH: 348 base pairs
- (B) TYPE: nucleic acid (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GTGAAGCTGC	AGGAGTCTGG	ACCTGAGCTG	GTGAAGCCTG	GGGCCTCAGT	GAAGATTTCC	60
TGCAAGGCTT	CTGGCTATGC	ATTCAGTAGC	TCCTGGATGA	ACTGGGTGAA	ACAGAGGCCT	120
GGGAAGGGTC	TTGAGTGGAT	TGGACGGATT	TATCCTGTAA	ATGGAGATAC	TAACTACAAT	180
GGGAAGTTCA	AGGGCAAGGC	CACACTGACT	GCAGACAAAT	CCTCCAGCAC	AGCCTACATG	240
CAACTCAGCA	GCCTGACATC	TGAGGACTCT	GCGGTCTACT	TCTGTGCAAC	CGATGGTTAC	300
TGGTACTTCG	ATGTCTGGGG	CCAAGGGACC	ACGGTCACCG	TCTCCTCA		348

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 118 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln Ser

Leu Ser Leu Thr Cys Ser Val Thr Gly Tyr Ser Ile Thr Ser Gly Tyr

Tyr Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu Trp Met

Gly Tyr Ile Ser Tyr Asp Gly Ser Asn Asn Tyr Asn Pro Ser Leu Lys

Asn Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Phe Phe Leu 70 75 80

Lys Leu Asn Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr Tyr Cys Ala

va	ı Tyr	Tyr	19r 100	Asp	GIÀ	ser	Ser	105	Asp	Tyr	Trp	GIY	110	Gly	Thr	
Th	r Val	Thr 115	Val	Ser	Ser											
(2) INF	ORMAT	ION 1	FOR S	SEQ :	ID N	0:12	:									
(i	(B (C	UENCI) LEI) TYI) STI) TOI	NGTH PE: 1 RANDI	: 354 nucle EDNE	4 ba: eic a SS: 0	se pa acid doub	airs									
(ii) MOL	ECULI	E TY	PE: (cDNA	to r	mRNA									
(xi) SEQ	UENCI	E DES	SCRI	PTIO	N: SI	EQ II	ои с	:12:							
GTGCAGC	IGC A	GGAG'	rctg(G AC	CTGG	CCTC	GTG	AAAC	CTT (CTCAC	STCT	CT G	rctc:	rcac(C	60
TGCTCTG	rca c	TGGC	TACT	C CA	rcac(CAGT	GGT:	TATTA	ACT (GGAA	CTGG	AT C	CGGC	AGTT	Г	120
CCAGGAA	ACA A	ACTG	GAAT(G GA	rggg(CTAC	ATA	AGCT	ACG A	ATGGT	TAGC	AA TA	AACT	ACAA	C	180
CCATCTC	rca a	AAAT	CGAA'	r cr	CCAT	CAC,T	CGT	GACA	CAT (CTAAC	GAAC	CA G	rttt:	rcct(3	240
AAGTTGA	ATT C	TGTG	ACTA	C TG	AGGA	CACA	GCCZ	ACATA	ATT A	ACTGT	rgcco	GT T	TATT	ACTA	C	300
GATGGTA	GCT C	TTTT	GACT	A CTO	GGGG	CCAA	GGG	ACCA	CGG :	CAC	CGTCT	rc c	rca			354
(2) INF	DRMAT	ION I	FOR S	SEQ :	ID N	0:13	:									
(i	(B (C	UENCI) LEI) TYI) STI) TOI	NGTH PE: 6 RANDI	: 112 amino EDNES	2 am: 5 ac: 5S: 4	ino a id sing!	acids	5								
(ii) MOL	ECULI	E TYI	PE: 1	pept:	ide										
(xi) SEQ	UENCI	E DES	SCRII	PTIO	N: SI	EQ II	ON C	:13:							
As _]	o Ile	Val	Leu	Thr 5	Gln	Ser	Pro	Ala	Ser 10	Leu	Ala	Val	Ser	Leu 15	Arg	
Gl	n Arg	Ala	Thr 20	Ile	Ser	Cys	Arg	Ala 25	Ser	Glu	Gly	Val	Asp 30	Ser	Tyr	
Gl	y Ile	Ser 35	Phe	Met	His	Trp	Tyr 40	Gln	Gln	Lys	Pro	Gly 45	Gln	Pro	Pro	
Ly	s Leu 50	Leu	Ile	Tyr	Arg	Ala 55	Ser	Tyr	Leu	Lys	Ser 60	Gly	Val	Pro	Ala	
` Ar	g Phe	Ser	Gly	Ser	Gly 70	Ser	Arg	Thr	Asp	Phe 75	Thr	Leu	Thr	Ile	Asp 80	
Pro	o Val	Glu	Ala	Asp 85	Asp	Ala	Ala	Thr	Tyr 90	Tyr	Cys	Gln	Gln	Asn 95	Asn	
Gl	ı Asp	Pro	Trp	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Arg	

(2)

100	105	•	110

(2) INFOR	TAMS	ION I	FOR S	SEQ :	ID NO	0:14	:								
(i)	(A) (B) (C)	LEI TYI STI	E CHANGTHE PE: 1 RANDI POLOG	: 336 nucle EDNES	6 bas eic a 88: 0	se pa acid doub	airs								
(ii)	MOLI	ECULI	E TYI	PE: 0	DNA	to r	nRNA							•	
(xi)	SEQU	JENCI	E DES	SCRII	OITS	N: SI	EQ II	ONO:	:14:						
GACATTGTG										CTCTA	AAGGG	CA GA	AGGGG	CAC	2
ATATCCTGC	CA GA	AGCCZ	AGTGA	A AGO	GTGTT	rgat	AGT	ratgo	GCA :	TAG	TTTT	AT GO	CACTO	GTAC	2
CAGCAGAAA	C C	AGGA	CAGC	C ACC	CCAA	ACTC	CTC	ATCT	ATC (STGC	ATCCI	ra co	CTAAA	ATCI	[
GGGGTCCCI	G C	CAGG	rtcac	TGC	GTAGT	rggg	TCT	AGGA	CAG A	ACTTO	CACCO	CT CA	ACCAI	TGAT	
CCTGTGGAG	G CI	GATO	GATGO	TGC	CAAC	CTAT	TACT	rgtc <i>i</i>	AGC A	LAAA	TAATO	A GO	ATCO	GTGC	3
ACGTTCGGT	G G	AGGCZ	ACCAZ	A GCI	rgga <i>i</i>	ATC	AAA	CGG							
(2) INFOR	TAM	ON I	FOR S	SEQ]	D NO):15	:								
(i)	(A) (B) (C)	LEN TYI STI	E CHA NGTH: PE: a RANDE POLOC	: 117 amino EDNES	7 ami o aci SS: s	ino a id singl	acids	3							
(ii)	MOLE	CULE	E TYP	E: p	pepti	lde									
(xi)	SEQU	JENCE	E DES	CRIE	OIT	l: SI	EQ II	NO:	15:						
Val 1	Gln	Leu	Gln	Glu 5	Ser	Gly	Ala	Glu	Pro 10	Ala	Lys	Pro	Gly	Ala 15	Ser
Val	Lys	Met	Ser 20	Cys	Lys	Ala	Ser	Gly 25	Tyr	Thr	Phe	Thr	Thr 30	Tyr	Trp
Met	His	Trp 35	Val	Lys	Gln	Arg	Pro 40	Gly	Gln	Gly	Leu	Glu 45	Trp	Ile	Gly
Tyr	Ile 50	Asn	Pro	Ser	Ser	Gly 55	Tyr	Thr	Glu	Tyr	Asn 60	Gln	Lys	Phe	Lys
Asp 65	Lys	Ala	Thr	Leu	Thr 70	Ala	Asp	Lys	Ser	Ser 75	Ser	Thr	Ala	Tyr	Met 80
Gln	Leu	Ile	Ser	Leu 85	Thr	Ser	Glu	Asp	Ser 90	Ala	Val	Tyr	Tyr	Cys 95	Ala
Arg	Arg	Gly	Asn 100	Tyr	Tyr	Tyr	Phe	Asp 105	Tyr	Trp	Gly	Gln	Gly 110	Thr	Thr

Val Thr Val Ser Ser

(2) INFORMATION FOR SEQ ID NO:16:												
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 351 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 												
(ii) MOLECULE TYPE: cDNA to mRNA												
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:												
GTGCAGCTGC AGGAGTCTGG GGCTGAACCG GCAAAACCTG GGGCCTCAGT GAAGATGTCC												
TGCAAGGCTT CTGGCTACAC CTTTACTACC TACTGGATGC ACTGGGTAAA ACAGAGGCCT												
GGACAGGGTC TGGAATGGAT TGGATACATT AATCCTAGCA GTGGTTATAC TGAGTACAAT												
CAGAAGTTCA AGGACAAGGC CACATTGACT GCAGACAAAT CCTCCAGCAC AGCCTACATG												
CAACTAATCA GCCTGACATC TGAGGACTCT GCAGTCTATT ACTGTGCAAG AAGGGGTAAT												
TACTACTACT TTGACTACTG GGGCCAAGGG ACCACGGTCA CCGTCTCCTC A												
(2) INFORMATION FOR SEQ ID NO:17:												
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 105 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 												
(ii) MOLECULE TYPE: peptide												
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:												
Asp Val Leu Met Thr Gln Thr Pro Lys Phe Leu Pro Val Ser Ala Gly 1 10 15												
Asp Arg Val Thr Met Thr Cys Lys Ala Ser Gln Ser Val Gly Asn Asn 20 25 30												
Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile 35 40 45												
Tyr Tyr Thr Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly 50 60												
Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Val Gln Val 65 70 75 80												
Glu Asp Leu Ala Val Tyr Phe Cys Gln Gln His Tyr Ser Ser Pro Tyr												

(2) INFORMATION FOR SEQ ID NO:18:

Thr Phe Gly Ser Gly Thr Lys Leu Glu 100 $\,$ 105

(ii)	MOL	ECULI	E TYI	PE: (cDNA	to r	nRNA								
(xi)	SEQ	JENCI	E DES	SCRI	PTIO	N: SI	EQ II	ои с	:18:						
GATGTTTT	GA T	GACC	CAAA	C TC	CAAA	ATTC	CTG	CCTG:	TAT (CAGC	AGGA	GA C	AGGG:	TAC	C
ATGACCTG	CA A	GGCC2	AGTC	A GA	GTGT	GGT	AATA	AATG:	rgg (CCTG	GTAC	CA A	CAGA	AGCC	A
GGACAGTC	TC C	raaa(CTGC:	r ga	CATA	CTAT	ACA	rcca/	ATC (GCTA	CACT	GG A	GTCC	CTGAT	r
CGCTTCAC	TG G	CAGT	GGAT	C TG	GGAC	AGAT	TTC	ACTT:	rca (CCAT	CAGC	AG TO	GTGC	AGGTT	r
GAAGACCT	GG C	AGTT	ratt:	г ст	GTCA	GCAG	CAT	CATA	GCT (CTCC	STATA	AC G	rtcg	GATCO	3
GGGACCAA	GC T	GGAG													
(2) INFO	RMAT:	ION I	FOR S	SEQ :	ID NO	0:19	:								
(i)	(B)	LEI TYI STI	NGTH: PE: & RANDI	: 12: amino EDNES	TERIS Lami Daci SS: s lines	ino a id singl	acids	5							
(ii)	MOLI	ECULI	Е ТҮІ	PE: p	pepti	ide					•				
(xi)	SEQU	JENCI	E DES	SCRI	OITS	1: SE	EQ II	ON C	:19:						
Gln 1	Val	Gln	Leu	Gln 5	Gln	Ser	Gly	Pro	Glu 10	Leu	Val	Lys	Pro	Gly 15	Ala
	Val	Lys	Ile 20	Ser	Cys	Lys	Ala	Ser 25	Gly	Tyr	Ala	Phe	Ser 30	Ser	Ser
Trp	Met	Asn 35	Trp	Val	Lys	Gln	Arg 40	Pro	Gly	Lys	Gly	Leu 45	Glu	Trp	Ile
Gly	Arg 50	Ile	Tyr	Pro	Gly	Asp 55	Gly	Asp	Thr	Asn	Asp 60	Asn	Gly	Lys	Phe
Lys 65	Gly	Lys	Ala	Thr	Leu 70	Thr	Ala	Asp	Lys	Ser 75	Ser	Ser	Thr	Ala	Tyr 80
Met	Gln	Leu	Ser	Ser 85	Leu	Thr	Ser	Glu	Asp 90	Ser	Ala	Val	Tyr	Phe 95	Сув
Ala	Arg	Ser	Tyr 100	Tyr	Tyr	Asp	Gly	Ser 105	Pro	Trp	Phe	Thr	Tyr 110	Trp	Gly
Gln	Gly	Thr 115	Leu	Val	Thr	Val	Ser 120	Ala			-				
(2) INFO	RMAT	ON I	OR S	SEQ I	D NO	0:20:	:								

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 315 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(i) SEQUENCE CHARACTERISTICS:

(xi)	SEQU	ENCE	DES	CRIE	OITS	1: SI	EQ II	ОИС	20:							
CAGGTTCAG	C TG	CAGC	AGTO	TGO	SACC1	rgag	CTG	GTGA/	AGC (CTGG	GCCI	C A	GTGAZ	AGATT	r	60
TCCTGCAAG	G CT	TCTG	GCTA	TGC	CATTO	CAGT	AGC	rccto	GA :	rgaa(CTGGG	T G	AAGC	AGAGO	3	120
CCTGGAAAG	G GT	CTTG	AGTG	GA1	TCG	ATT	TAT	CCTG	GAG A	ATGG	GATA	C T	AACG/	CAA	C	180
GGGAAGTTC	A AG	GGAG	GCAA	GGC	CCACA	ACTG	ACC	GCAG	ACA A	AATC	CTCCA	G C	ACAG	CCTA	C	240
ATGCAACTC	A GC	AGTO	TGAC	ATC	CTGAC	GAC	TCT	GCGGT	CT A	ACTTO	CTGTG	C A	AGAT	CGTAT	r	300
TACTACGAT	G GT.	AGCC	CCTG	GTI	TACI	TAC	TGG	GCCZ	AAG (GGACT	CTGG	T C	ACTG:	CTC	r	360
GCA																363
(2) INFOR	MATI	ON F	OR S	EQ I	D NO):21:	:									
(i)	(B) (C)	LEN TYP STR	GTH: E: a ANDE	108 mino DNES	ami aci	ino a id singl	acids	5		•						
(ii) (xi)				-	-		iQ II	O NO:	21:							
Asp 1	Ile	Gln	Met	Thr 5	Gln	Thr	Thr	Ser	Ser 10	Leu	Ser	Ala	Ser	Leu 15	Gly	
Asp	Arg '	Val	Thr 20	Ile	Ser	Cys	Arg	Ala 25	Ser	Gln	Asp	Ile	Ser 30	Asn	Tyr	
Leu	Asn '	Trp 35	Tyr	Gln	Gln	Lys	Pro 40	Asp	Gly	Thr	Val	Lys 45	Leu	Leu	Ile	
	Tyr ' 50	Thr	Ser	Arg	Leu	His 55	Ser	Gly	Val	Pro	Ser 60	Arg	Phe	Ser	Gly	
Ser 65	Gly	Ser	Gly	Thr	Asp 70	Tyr	Ser	Leu	Thr	Ile 75	Ser	Asn	Leu	Glu	Pro 80	
Glu	Asp	Ile	Ala	Thr 85	Tyr	Phe	Cys	Gln	Gln 90	Tyr	Ser	Glu	Phe	Pro 95	Trp	
Thr	Phe (Gly	Gly 100	Gly	Thr	Lys	Leu	Glu 105	Ile	Lys	Arg					

(A) LENGTH: 363 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double

(D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA to mRNA

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 324 base pairs (B) TYPE: nucleic acid

(XI)	SEQ	UENC	E DES	SCRII	PTIO	N: SI	EQ II	ON C	:22:						
GATATCCA	GA T	GACA	CAGA	CTAC	CATC	CTCC	CTG	rctgo	CCT (CTCTC	GGA	GA C	AGAG	CAC	2
ATCAGTTG	CA G	GGCA <i>l</i>	AGTC	A GG	TAT	ragc	AAT	ratt?	raa 2	ACTGO	TAT	CA GO	CAGA	AACC	A
GATGGAAC'	rg T	TAAA	CTCC	r ga:	CTA	CTAC	ACA:	rcaa(GAT S	raca(CTCAC	GG A	GTCC	CATC	A
AGGTTCAG	IG G	CAGT	GGT	C TGC	GGAC	AGAT	TAT	rctc:	CA (CCATO	CAGC	AA C	CTGG	AACCI	r
GAAGATAT	rg c	CACT	ract:	r TTC	GTCA	GCAA	TATA	AGTGA	AAT :	TCCC	GTGG/	AC G	TTCG	GTGG!	A
GGCACCAA	GC T	GGAA	ATCAZ	A ACC	GG										
(2) INFO	RMAT	ION 1	FOR S	SEQ :	ID NO	0:23	:								
(i)	(A) (B) (C)	UENCI) LEI) TYI) STI) TOI	NGTH PE: 6 RANDI	: 119 amino EDNES	e ami o aci	ino a id sing:	acids	5							
(ii)	MOLI	ECULI	E TYI	PE: p	pepti	ide						•			
(xi)	SEQ	JENCI	E DES	SCRIE	OITS	1: SI	EQ II	ON C	:23:						
Gln 1	Val	His	Leu	Gln 5	Gln	Ser	Gly	Ala	Glu 10	Leu	Val	Arg	Pro	Gly 15	Thr
Ser	Val	Lys	Met 20	Ser	Cys	Lys	Ala	Ala 25	Gly	Tyr	Thr	Phe	Thr 30	Asn	Tyr
Trp	Ile	Gly 35	Trp	Val	Lys	Gln	Arg 40	Pro	Gly	His	Gly	Leu 45	Glu	Trp	Ile
Gly	Tyr 50	Leu	Tyr	Pro	Gly	Gly 55	Leu	Tyr	Thr	Asn	Tyr 60	Asn	Glu	Lys	Phe
Lys 65	Gly	Lys	Ala	Thr	Leu 70	Thr	Ala	Asp	Thr	Ser 75	Ser	Ser	Thr	Ala	Tyr 80
Met	Gln	Leu	Ser	Ser 85	Leu	Thr	Ser	Glu	Asp 90	Ser	Ala	Ile	Tyr	Tyr 95	Cys
Ala	Arg	Tyr	Arg 100	Asp	Tyr	Asp	Tyr	Ala 105	Met	Asp	Tyr	Trp	Gly 110	Gln	Gly
Thr	Ser	Val 115	Thr	Val	Ser	Ser									
(2) INFO	ЗМАТ.	TON I	FOR S	SEO I	או מו	1.24	•								

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 357 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D)	TOPOLOGY:	linear
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(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

(,			- 2 2 1,0,21,	•		
CAGGTCCAC	TGCAGCAGTC	TGGAGCTGAG	CTGGTAAGGC	CTGGGACTTC	AGTGAAGATG	60
TCCTGCAAGO	CTGCTGGATA	CACCTTCACT	AACTACTGGA	TAGGTTGGGT	AAAGCAGAGG	120
CCTGGACATO	GCCTTGAGTG	GATTGGATAT	CTTTACCCTG	GAGGTCTTTA	TACTAACTAC	180
AATGAGAAGI	TCAAGGGCAA	GGCCACACTG	ACTGCAGACA	CATCCTCCAG	CACAGCCTAC	240

300

357

ATGCAGCTCA GCAGCCTGAC ATCTGAGGAC TCTGCCATCT ATTACTGTGC AAGATACAGG

GATTACGACT ATGCTATGGA CTACTGGGGT CAAGGAACCT CAGTCACCGT CTCCTCA

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Asp Val Val Leu Thr Gln Thr Pro Leu Ser Leu Pro Val Asn Ile Gly

Asp Gln Ala Ser Ile Ser Cys Lys Ser Thr Lys Ser Leu Leu Asn Ser

Asp Gly Phe Thr Tyr Leu Gly Trp Cys Leu Gln Lys Pro Gly Gln Ser

Pro Gln Leu Leu Ile Tyr Leu Val Ser Asn Arg Phe Ser Gly Val Pro

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Phe Gln Ser 90

Asn Tyr Leu Pro Leu Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys

Arg

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 339 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:	
GATGTTGTTC TGACCCAAAC TCCACTCTCT CTGCCTGTCA ATATTGGAGA TCAAGCCTCT	60
ATCTCTTGCA AGTCTACTAA GAGCCTTCTG AATAGTGATG GATTCACTTA TTTGGGCTGG	120
TGCCTGCAGA AGCCAGGCCA GTCTCCACAG CTCCTAATAT ATTTGGTTTC TAATCGATTT	180
TCTGGAGTTC CAGACAGGTT CAGTGGTAGT GGGTCAGGGA CAGATTTCAC CCTCAAGATC	240
AGCAGAGTGG AGGCTGAGGA TTTGGGAGTT TATTATTGCT TCCAGAGTAA CTATCTTCCT	300
CTTACGTTCG GATCGGGGAC CAAGCTGGAA ATAAAACGG	339
(2) INFORMATION FOR SEQ ID NO:27:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 117 amino acids (B) TYPE: amino acid	
(C) STRANDEDNESS: single	

(ii) MOLECULE TYPE: peptide

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala 1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Ser 20 25 30

Trp Met Asn Trp Val Lys Gln Arg Pro Gly Lys Gly Leu Glu Trp Ile 35 40

Gly Arg Ile Tyr Pro Val Asn Gly Asp Thr Asn Tyr Asn Gly Lys Phe 50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr 65 70 75 80

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys 85 90 95

Ala Thr Asp Gly Tyr Trp Tyr Phe Asp Val Trp Gly Ala Gly Thr Thr
100 105 110

Val Thr Val Ser Ser 115

- (2) INFORMATION FOR SEQ ID NO:28:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 351 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA to mRNA

(xi) SI	EQUENCE DESC	CRIPTION: SE	EQ ID NO:28	1		
CAGGTTCAGC	TGCAGCAGTC	TGGACCTGAG	CTGGTGAAGC	CTGGGGCCTC	AGTGAAGATT	60
TCCTGCAAGG	CTTCTGGCTA	TGCATTCAGT	AGCTCCTGGA	TGAACTGGGT	GAAACAGAGG	120
CCTGGGAAGG	GTCTTGAGTG	GATTGGACGG	ATTTATCCTG	TAAATGGAGA	TACTAACTAC	180
AATGGGAAGT	TCAAGGGCAA	GGCCACACTG	ACTGCAGACA	AATCCTCCAG	CACAGCCTAC	240
ATGCAACTCA	GCAGCCTGAC	ATCTGAGGAC	TCTGCGGTCT	ACTTCTGTGC	AACCGATGGT	300
TACTGGTACT	TCGATGTCTG	GGGCGCAGGG	ACCACGGTCA	CCGTCTCCTC	A	351

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 108 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Asn Ile Val Met Thr Gln Ser Pro Lys Ser Met Ser Met Ser Val Gly

Glu Arg Val Thr Leu Ser Cys Lys Ala Ser Glu Asn Val Asp Ile Tyr 25

Val Ser Trp Tyr Gln Gln Lys Pro Glu Gln Ser Pro Lys Leu Leu Ile

Tyr Gly Thr Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly

Ser Gly Ser Ala Thr Asp Phe Thr Leu Thr Ile Ser Asn Val Gln Ala

Glu Asp Leu Ser Asp Tyr Tyr Cys Val Gln Ser Tyr Ser Tyr Pro Trp

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 324 base pairs(B) TYPE: nucleic acid

 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

AACATTGTAA	TGACCCAATC	TCCCAAATCC	ATGTCCATGT	CAGTAGGAGA	GAGGGTCACC	60
TTGAGCTGCA	AGGCCAGTGA	GAATGTGGAT	ATTTATGTAT	CCTGGTATCA	ACAGAAACCA	120
GAGCAGTCTC	CTAAACTGCT	GATATACGGG	ACATCCAACC	GGTACACTGG	GGTCCCCGAT	180
CGCTTCACAG	GCAGTGGATC	TGCAACAGAT	TTCACTCTGA	CCATCAGCAA	TGTGCAGGCT	240
GAAGACCTTT	CAGATTATTA	CTGTGTACAG	AGTTACAGCT	ATCCGTGGAC	ATTCGGTGGA	300
GGCACCAAGC	TGGAAATCAA	ACGG				324

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Leu Ser His Lys Val Tyr Met Arg Asn Ser Lys Tyr Pro Gln